VERSION WITH MARKINGS TO SHOW CHANGES MADE

IN THE SPECIFICATION

[0009] Sets of probes designed for the methods of the present invention are also provided by the invention. Thus, the invention provides *e.g.*, a set of mixed homologous probes for detection of at least one allelic variant of a nucleic acid family, wherein at least one of the probes is non-linear, the probes comprise sequences that are completely complementary to and are specific for one of the allelic variants of the family, except for a specific mismatch located upstream and/or downstream from the site of variation. As used herein, a *non-linear probe* means a probe, considered as a single strand, wherein base pairing within the molecule can fix the location of one region relative to another.

IN THE CLAIMS:

1. (Twice Amended) A method for reducing background signals in a hybridization reaction of nucleic acids involving at least two homologous probes, wherein at least one of the two homologous probes is a non-linear probe, said method comprising:

introducing a mismatch with an intended target sequence in said non-linear probe; and

conducting a single hybridization reaction using said at least two homologous probes, thereby reducing the background signals of the hybridization reaction.

2. (Twice Amended) A method for reducing background signals in a hybridization reaction of nucleic acids involving at least two homologous target sequences, said method comprising:

providing for an intended mismatch between at least one of the two homologous target sequences and at least one non-linear probe; and

conducting a single hybridization reaction using said at least two homologous target sequences, thereby reducing the background signals of the hybridization reaction.